



## Genome wide association and genomic selection to speed up genetic improvement for meat quality and yield in Hanwoo

Seung-Hwan Lee<sup>1</sup>, Bong-Hwan Choi<sup>2</sup>, Da-Jeong Lim<sup>2</sup>, Chang-Gwon Dang<sup>1</sup>, Hyeong-Cheol Kim<sup>1</sup>, Seong-Hum Yeon<sup>1</sup>, Hee-Sul Kang<sup>1</sup>, and Boh-Seok Yang<sup>1</sup>

National Institute of Animal Science, RDA

[slee46@korea.kr](mailto:slee46@korea.kr)



**Abstract** - Genomic prediction of cattle's genetic merit using dense SNP panels is available for estimation of genomic breeding values (GEBV) to

select superior young bulls in livestock. In genomic selection, the estimation of genomic breeding values is predicted to sum up all loci that are estimated based on phenotypes and genotypes in training population. This is particularly useful for traits that are very difficult to measure, such as marbling (MS). The accuracy of these genomic predictions depends on the genetic architecture of the complex traits. For example, number of loci affecting the trait and distribution of their effects.

Here we reported that genome wide association test to detect significant loci affecting marbling score (MS), carcass weight (CWT), eye muscle area (EMA) and backfat thickness (BF), and their



effects contributing to total additive genetic variation. The GWAS identified one major chromosome region ranging 23 Mb to 25 Mb on chromosome 14, which is associated with carcass weight in Hanwoo. The Bonferroni-corrected genome wide significant association ( $P < 1.52 \times 10^{-6}$ ) were detected for 6 SNPs for carcass weight on chromosome 14. The other carcass traits such as EMA, BF and MAR were not detected in any SNP markers that met Bonferroni-corrected threshold

( $P < 1.52 \times 10^{-6}$ ). The distribution of effects for the carcass traits (CWT, EMA, MS and BF) was estimated



and the most significant SNPs for CWT accounted for 6.73 to 10.55 % of additive genetic variance, which is quite large proportion against total additive genetic variance. However, significant SNP explained moderate amount of

additive genetic variance in the other carcass traits (EMA, MS and BF). As results, genetic architecture for the carcass traits seems to have few loci with larger effects controlling carcass weight, while many loci with small effects are still contributing the total additive genetic variance in Hanwoo. With this discovery dataset for GWAS (n=1,011), we predicted genomic breeding value (GEBV) of three different selection population (Sire without obs (n=106), Progeny without obs (n=178) and young cow without obs (n=236) using genomic BLUP method. Accuracy of GEBV was accurately estimated in Sire without obs (70%), while the other two populations showed a little bit lower accuracy of GEBV (27-38%). However, given that their relatedness with GWAS dataset (Sire; 0.5, Progeny; 0.1-0.2 and cow; 0.05) and reference population size, it was considerably accurately estimated in Hanwoo. In conclude, genomic prediction will be working well and it will drive to speed up genetic improvement in Hanwoo.



**KeyWords:** Genomic Prediction, Genome wide Association, Breeding Value, IMF, MS and CWT

<sup>1</sup>Hanwoo Experiment Station, National Institute of Animal Science, RDA, PyeongChang 232-950, Korea

<sup>2</sup>Animal Genome & Bioinformatics Division, National Institute of Animal Science, RDA, Suwon 441-706, Korea

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